

A UNIQUE EVOLUTION



Biologist Robert Wayne and his research team mix old-fashioned detective work and sophisticated technology in their studies of genes in wolves and dogs.

By Aaron Dalton

For most observers, the black wolves that roam Yellowstone National Park are animals to be admired as symbols of power and beauty, and appreciated for their role in maintaining the natural balance in the environment.

For UCLA evolutionary biology professor Robert Wayne, North American black wolves represent something very different—an unprecedented evolution of a gene in the wild that had originated in domestic animals.

Research by Wayne and his colleagues at the UCLA Conservation Genetics Resource Center indicates that black wolves inherited their dark coats from domesticated dogs, most likely dogs that lived with Native Americans approximately 12,000 years ago.

How did Wayne, a professor in the Department of Ecology and Evolutionary Biology, and his fellow researchers identify the gene that causes the black coat and arrive at the estimate of when the gene crossed from dogs to wolves? The answer to that question involves a mix of old-fashioned detective work and sophisticated technology.

In the field, graduate student Dan Stahler travels across the winter Yellowstone terrain on cross-country skis at -30 degrees, gathering DNA samples from Yellowstone's wolves after they have been tranquilized, fit with temporary radio collars, and then tracked from the air. Back in Wayne's laboratory, graduate student Bridgett vonHoldt scans Stahler's samples using genotyping 'chips'—bits of synthesized DNA that are actually printed onto little squares of plastic called arrays and analyzed for the presence of 127,000 genetic markers.

Information gathered by Wayne's team is shared with researchers worldwide as part of the CanMap project that is mapping all genetic variations in dogs.

Why do canines merit such intensive genetic research?

"When it comes to human genetic diseases, it turns out that dogs have more analogs than any other species," said Wayne. "By mapping genetic variability in dogs, we hope to learn something about the genetic basis of diseases like cancer that may ultimately benefit humans."

Back to the black-coated North American wolves—the genetic data paired with a detailed family tree for wolves showed that the black coloration seemed linked to a single dominant gene. If a wolf with the gene for a black coat mated with a wolf that had the grey coat gene, a black coat resulted in a way that should seem familiar to anyone who remembers high school biology and Gregor Mendel's experiments with pea cultivation.

At a conference in Holland, Wayne learned that a gene called "K locus" had just been discovered to control coat coloration in dogs. What if the gene that gave dogs their black coats was doing the same for North American wolves? Turning to the data, Wayne found that K locus was indeed the answer.

The next question was when K locus began to appear in wolves. To figure out when a particular genetic sequence first enters a genome, researchers look at variability near the gene. In dogs, a fair amount of variability and genetic "rescrambling" near the K locus gene indicated that there had been ample time for the gene to mutate.

In wolves, there was far less variation around the K locus gene, suggesting that the gene had entered the population more recently and then spread rapidly in a phenomenon known as "selective sweep." (The human genetic sequence also has examples of selective sweep. For example, the genetic code for lactose tolerance that allows adults



Robert Wayne and graduate student Bridgett vonHoldt.

to digest milk swept into high frequency among Europeans when they began cultivating dairy herds.)

Looking at the number of differences between the gene that causes black coats and the one that codes for grey coats, Wayne estimates that the black coat gene entered the wolf population through Native American dogs some 12,000 or more years ago.

Meanwhile, the conservation work done at the UCLA Conservation Genetics Resource Center also plays a role in determining public policy. Scientists associated with the Center look into the dynamics of mating, reproduction patterns, and genetic variability among Yellowstone wolves to determine how genes flow among wolf

populations in the national park. Their research shows a lack of "genetic communication" among Yellowstone wolves and other populations in Idaho and Montana. Environmental groups have used these findings in their attempts to stop the removal of the wolf from the Endangered Species list, arguing that numerical recovery should carry less weight in light of limited genetic communication among populations.

Why do populations need genetic diversity?

"In the near term, inbreeding associated with a lack of genetic variability can lead to lower reproductive rates," said Wayne.

In extreme cases, such as with the near-extinct Florida panther, a deficiency of genetic variability meant the population simply could not reproduce on its own. Only the introduction of some mountain lions from Texas provided a fresh genetic infusion that enabled reproduction and saved the population from certain extinction.

The UCLA Conservation Genetics Resource Center directed by John Pollinger now tackles conservation-related projects involving not just wolves, but also other endangered species like the Palos Verdes butterfly and red abalone.

"The red abalone has become so endangered that a commercial harvest is now allowed from only one location," said Wayne. "But say that a truckload of red abalone is pulled over. How can you tell if the abalone was taken from a legal zone?"

"Before there was no way of testing where the catch came from, but we have been developing a genetic test that allows you to take an abalone found in the market, in a truck or even the scraping of a shell and figure out whether that abalone is legal or not. That's one example of conservation genetics at work in law enforcement forensics." 

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